#5

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        RAW SEQUENCE LISTING              DATE: 10/29/2001
        PATENT APPLICATION:  US/09/927,850   TIME: 15:41:28

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  3 <110> APPLICANT: Welcher, Andrew
  4        Wen, Duanzhi
  5        Kelly, Michael
  7 <120> TITLE OF INVENTION: Interferon-Like Molecules and Uses Thereof
  9 <130> FILE REFERENCE: 99,372-F
 11 <140> CURRENT APPLICATION NUMBER: 09/927,850
 12 <141> CURRENT FILING DATE: 2001-08-10
 14 <150> PRIOR APPLICATION NUMBER: 09/724,860
 15 <151> PRIOR FILING DATE: 2000-11-28
 17 <150> PRIOR APPLICATION NUMBER: 60/169,720
 18 <151> PRIOR FILING DATE: 1999-12-08
 20 <160> NUMBER OF SEQ ID NOS: 39
 22 <170> SOFTWARE: PatentIn Ver. 2.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 913
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Rattus norvegicus
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 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (53)..(625)
 33 <220> FEATURE:
 34 <221> NAME/KEY: sig_peptide
 35 <222> LOCATION: (53)..(115)
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 39                                                              Met Thr
 40                                                               1
 42 ctg aag tat tta tgg ctg gtg gcc ctc gtg gct cta tac att tca ccc  106
 43 Leu Lys Tyr Leu Trp Leu Val Ala Leu Val Ala Leu Tyr Ile Ser Pro
 44         5                   10                  15
 46 atc cag tct cag aac tgt gtg tat ctg gat cat acc atc ttg gaa aac  154
 47 Ile Gln Ser Gln Asn Cys Val Tyr Leu Asp His Thr Ile Leu Glu Asn
 48      20                  25                  30
 50 atg aaa ctt ctg agc agc atc agg acc acc ttt ccc tta aga tgt cta  202
 51 Met Lys Leu Leu Ser Ser Ile Arg Thr Thr Phe Pro Leu Arg Cys Leu
 52   35                  40                  45                  50
 54 aaa gat atc acg gat ttt gag ttt cct caa gag att ctg ctg tac gtc  250
 55 Lys Asp Ile Thr Asp Phe Glu Phe Pro Gln Glu Ile Leu Leu Tyr Val
 56                  55                  60                  65
 58 cag cat gtg aaa aag gac ata aag gca gtc acc tat cat ata tct tct  298
 59 Gln His Val Lys Lys Asp Ile Lys Ala Val Thr Tyr His Ile Ser Ser
 60                  70                  75                  80
 62 ctg gcg cta att att ttc agt ctt aaa gac tcc atc tcc ctg gcg aca  346
 63 Leu Ala Leu Ile Ile Phe Ser Leu Lys Asp Ser Ile Ser Leu Ala Thr
 64         85                  90                  95
 66 gag gaa cgc ttg gaa cgt atc aga tcg gga ctt ttc aaa caa gtg cag  394
 67 Glu Glu Arg Leu Glu Arg Ile Arg Ser Gly Leu Phe Lys Gln Val Gln
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10/29/01

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71 Gln Ala Arg Glu Cys Met Val Asp Glu Glu Asn Lys Asn Thr Glu Glu
72 115                    120                    125                    130
74 gac agt aca tca caa cat cct cac tca gag ggc ttc aag gca gtc tac   490
75 Asp Ser Thr Ser Gln His Pro His Ser Glu Gly Phe Lys Ala Val Tyr
76                    135                    140                    145
78 ctg gaa ttg aac aag tat ttc ttc aga atc aga aag ttc ctg gta aat   538
79 Leu Glu Leu Asn Lys Tyr Phe Phe Arg Ile Arg Lys Phe Leu Val Asn
80                    150                    155                    160
82 aag aaa tac agt ttc tgt gcc tgg aag att gtc gtg gtg gaa ata aga   586
83 Lys Lys Tyr Ser Phe Cys Ala Trp Lys Ile Val Val Val Glu Ile Arg
84           165                    170                    175
86 aga tgt ttc agt ata ttt tac aaa cta ctc aac atg aat tgagaatcat   635
87 Arg Cys Phe Ser Ile Phe Tyr Lys Leu Leu Asn Met Asn
88       180                    185                    190
90 ccagcttcaa gcaagaactt agatagaagt tgtgactgct caaatgtccc caagaacgct 695
92 tgattctaag gctattgcga gtctgctgct acacacttcg gacgcaagac ttttcaaggt 755
94 cagggttcaa ggtagtacag tcaaaggaag tcttatgtta agcaaaagaa aaatttcagt 815
96 ggaaaagcta gcagaaatgt caacttgtca aaaaaacaac ttatggatta tggcattgac 875
98 gttactagca aaaaaataa aacaaaaaaa aacaaaaa                           913
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 191
103 <212> TYPE: PRT
104 <213> ORGANISM: Rattus norvegicus
106 <400> SEQUENCE: 2
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108   1           5                    10                    15
110 Ser Pro Ile Gln Ser Gln Asn Cys Val Tyr Leu Asp His Thr Ile Leu
111           20                    25                    30
113 Glu Asn Met Lys Leu Leu Ser Ser Ile Arg Thr Thr Phe Pro Leu Arg
114           35                    40                    45
116 Cys Leu Lys Asp Ile Thr Asp Phe Glu Phe Pro Gln Glu Ile Leu Leu
117       50                    55                    60
119 Tyr Val Gln His Val Lys Lys Asp Ile Lys Ala Val Thr Tyr His Ile
120   65                    70                    75                    80
122 Ser Ser Leu Ala Leu Ile Ile Phe Ser Leu Lys Asp Ser Ile Ser Leu
123                    85                    90                    95
125 Ala Thr Glu Glu Arg Leu Glu Arg Ile Arg Ser Gly Leu Phe Lys Gln
126                    100                    105                    110
128 Val Gln Gln Ala Arg Glu Cys Met Val Asp Glu Glu Asn Lys Asn Thr
129           115                    120                    125
131 Glu Glu Asp Ser Thr Ser Gln His Pro His Ser Glu Gly Phe Lys Ala
132       130                    135                    140
134 Val Tyr Leu Glu Leu Asn Lys Tyr Phe Phe Arg Ile Arg Lys Phe Leu
135 145                    150                    155                    160
137 Val Asn Lys Lys Tyr Ser Phe Cys Ala Trp Lys Ile Val Val Val Glu
138                    165                    170                    175
140 Ile Arg Arg Cys Phe Ser Ile Phe Tyr Lys Leu Leu Asn Met Asn
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Output Set: N:\CRF3\10292001\I927850.raw

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145 <211> LENGTH: 168
146 <212> TYPE: PRT
147 <213> ORGANISM: Rattus norvegicus
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151  1               5                  10                  15
153 Ser Ile Arg Thr Thr Phe Pro Leu Arg Cys Leu Lys Asp Ile Thr Asp
154             20                  25                  30
156 Phe Glu Phe Pro Gln Glu Ile Leu Leu Tyr Val Gln His Val Lys Lys
157           35                  40                  45
159 Asp Ile Lys Ala Val Thr Tyr His Ile Ser Ser Leu Ala Leu Ile Ile
160       50                  55                  60
162 Phe Ser Leu Lys Asp Ser Ile Ser Leu Ala Thr Glu Glu Arg Leu Glu
163  65                  70                  75                  80
165 Arg Ile Arg Ser Gly Leu Phe Lys Gln Val Gln Gln Ala Arg Glu Cys
166                 85                  90                  95
168 Met Val Asp Glu Glu Asn Lys Asn Thr Glu Glu Asp Ser Thr Ser Gln
169             100                 105                 110
171 His Pro His Ser Glu Gly Phe Lys Ala Val Tyr Leu Glu Leu Asn Lys
172           115                 120                 125
174 Tyr Phe Phe Arg Ile Arg Lys Phe Leu Val Asn Lys Lys Tyr Ser Phe
175       130                 135                 140
177 Cys Ala Trp Lys Ile Val Val Val Glu Ile Arg Arg Cys Phe Ser Ile
178 145                 150                 155                 160
180 Phe Tyr Lys Leu Leu Asn Met Asn
181                 165
184 <210> SEQ ID NO: 4
185 <211> LENGTH: 1836
186 <212> TYPE: DNA
187 <213> ORGANISM: Homo sapiens
189 <220> FEATURE:
190 <221> NAME/KEY: CDS
191 <222> LOCATION: (575)..(1195)
193 <220> FEATURE:
194 <221> NAME/KEY: sig_peptide
195 <222> LOCATION: (575)..(655)
197 <400> SEQUENCE: 4
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200 tcaaataatc acagtcattt ggtcaatgtc tatgattaac tcaatgagac aggatgtttg 120
202 gctatagcac caggtacaaa aaatatattt tcatgaagga tcactccctc ttatgtaata 180
204 gatttgggtg agtgagtgag tgagtgagtg catggactca cagcttttgg ctttctgaaa 240
206 taccctgcat cagtcttgtt atgatgattc cttagtgctg ggatggatca tccaggcatt 300
208 taaggtaaca cgatggtaat tctttgctca tttttcaggg aaaaaaaaaa gttatcactt 360
210 ccaaagtcgg catagtcacc cgaagtaaaa aaaaaaaaaa aaaaaaaaag cctcagaggc 420
212 aaaggaaagg ggccgcaacc ttggttaact gtgaaatgac gaatgagaaa actcctcctg 480
214 ctgaagatat tcaggtatat aaaggcacat gaaggaaaac tcaaaacatc attgtcatat 540
216 acacatcttc tggattttttt agcttgcaaa aaaa atg agc acc aaa cct gat atg 595
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PATENT APPLICATION: US/09/927,850   TIME: 15:41:28

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Output Set: N:\CRF3\10292001\I927850.raw

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218                                         1                 5
220 att caa aag tgt ttg tgg ctt gag atc ctt atg ggt ata ttc att gct   643
221 Ile Gln Lys Cys Leu Trp Leu Glu Ile Leu Met Gly Ile Phe Ile Ala
222         10                  15                  20
224 ggc acc cta tcc ctg gac tgt aac tta ctg aac gtt cac ctg aga aga   691
225 Gly Thr Leu Ser Leu Asp Cys Asn Leu Leu Asn Val His Leu Arg Arg
226     25                  30                  35
228 gtc acc tgg caa aat ctg aga cat ctg agt agt atg agc aat tca ttt   739
229 Val Thr Trp Gln Asn Leu Arg His Leu Ser Ser Met Ser Asn Ser Phe
230 40                  45                  50                  55
232 cct gta gaa tgt cta cga gaa aac ata gct ttt gag ttg ccc caa gag   787
233 Pro Val Glu Cys Leu Arg Glu Asn Ile Ala Phe Glu Leu Pro Gln Glu
234                 60                  65                  70
236 ttt ctg caa tac acc caa cct atg aag agg gac atc aag aag gcc ttc   835
237 Phe Leu Gln Tyr Thr Gln Pro Met Lys Arg Asp Ile Lys Lys Ala Phe
238             75                  80                  85
240 tat gaa atg tcc cta cag gcc ttc aac atc ttc agc caa cac acc ttc   883
241 Tyr Glu Met Ser Leu Gln Ala Phe Asn Ile Phe Ser Gln His Thr Phe
242         90                  95                  100
244 aaa tat tgg aaa gag aga cac ctc aaa caa atc caa ata gga ctt gat   931
245 Lys Tyr Trp Lys Glu Arg His Leu Lys Gln Ile Gln Ile Gly Leu Asp
246     105                 110                 115
248 cag caa gca gag tac ctg aac caa tgc ttg gag gaa gac gag aat gaa   979
249 Gln Gln Ala Glu Tyr Leu Asn Gln Cys Leu Glu Glu Asp Glu Asn Glu
250 120                 125                 130                 135
252 aat gaa gac atg aaa gaa atg aaa gag aat gag atg aaa ccc tca gaa   1027
253 Asn Glu Asp Met Lys Glu Met Lys Glu Asn Glu Met Lys Pro Ser Glu
254                 140                 145                 150
256 gcc agg gtc ccc cag ctg agc agc ctg gaa ctg agg aga tat ttc cac   1075
257 Ala Arg Val Pro Gln Leu Ser Ser Leu Glu Leu Arg Arg Tyr Phe His
258             155                 160                 165
260 agg ata gac aat ttc ctg aaa gaa aag aaa tac agt gac tgt gcc tgg   1123
261 Arg Ile Asp Asn Phe Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp
262         170                 175                 180
264 gag att gtc cga gtg gaa atc aga aga tgt ttg tat tac ttt tac aaa   1171
265 Glu Ile Val Arg Val Glu Ile Arg Arg Cys Leu Tyr Tyr Phe Tyr Lys
266     185                 190                 195
268 ttt aca gct cta ttc agg agg aaa taaggtatat ttttggaatt aaaattcctt  1225
269 Phe Thr Ala Leu Phe Arg Arg Lys
270 200                 205
272 ttccctccga aatctctttc tccttctcct cctccatctt cttttaagg attgttgtgc   1285
274 tgtcctgtaa gcctgtcctc agttggactg gtagcctcgg aacatcaggg acactcacct   1345
276 ctctaaggag aggtaatgcc aaccatcctc agggtgacca agagtctcct tagaaagtct   1405
278 ttaagacatt tttaaaggaa taagattccc tctccgtctt cttctattct ctcttgctct   1465
280 tttctgtggc cattttgaaa gagctttgct atatatacca cctgtggact tcaccaagac   1525
282 aatggctaga ggatagggag cagagaatgt tgcaaaatgg taacatttca atgacttaac   1585
284 tgttttgctg ccaaggttgc ttatcctatg aaaattcagc acattaaaag agcttataca   1645
286 tgctccctag agtcaatact cttgcatttt cccctcctg ctcgggggga aaaaggttga   1705
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RAW SEQUENCE LISTING
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Input Set : A:\99372Fseq.txt
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290 tttcattact ttaagagtga agatccatag tgaaattgga tggatggttg aattagacga 1825
292 ccattaagct t                                                       1836
295 <210> SEQ ID NO: 5
296 <211> LENGTH: 207
297 <212> TYPE: PRT
298 <213> ORGANISM: Homo sapiens
300 <400> SEQUENCE: 5
301 Met Ser Thr Lys Pro Asp Met Ile Gln Lys Cys Leu Trp Leu Glu Ile
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305             20                  25                  30
307 Leu Asn Val His Leu Arg Arg Val Thr Trp Gln Asn Leu Arg His Leu
308             35                  40                  45
310 Ser Ser Met Ser Asn Ser Phe Pro Val Glu Cys Leu Arg Glu Asn Ile
311     50                  55                  60
313 Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr Gln Pro Met Lys
314 65                  70                  75                  80
316 Arg Asp Ile Lys Lys Ala Phe Tyr Glu Met Ser Leu Gln Ala Phe Asn
317                 85                  90                  95
319 Ile Phe Ser Gln His Thr Phe Lys Tyr Trp Lys Glu Arg His Leu Lys
320             100                 105                 110
322 Gln Ile Gln Ile Gly Leu Asp Gln Gln Ala Glu Tyr Leu Asn Gln Cys
323             115                 120                 125
325 Leu Glu Glu Asp Glu Asn Glu Asn Glu Asp Met Lys Glu Met Lys Glu
326     130                 135                 140
328 Asn Glu Met Lys Pro Ser Glu Ala Arg Val Pro Gln Leu Ser Ser Leu
329 145                 150                 155                 160
331 Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe Leu Lys Glu Lys
332             165                 170                 175
334 Lys Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu Ile Arg Arg
335             180                 185                 190
337 Cys Leu Tyr Tyr Phe Tyr Lys Phe Thr Ala Leu Phe Arg Arg Lys
338             195                 200                 205
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342 <211> LENGTH: 178
343 <212> TYPE: PRT
344 <213> ORGANISM: Homo sapiens
346 <400> SEQUENCE: 6
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348  1               5                  10                  15
350 Arg His Leu Ser Ser Met Ser Asn Ser Phe Pro Val Glu Cys Leu Arg
351             20                  25                  30
353 Glu Asn Ile Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr Gln
354             35                  40                  45
356 Pro Met Lys Arg Asp Ile Lys Lys Ala Phe Tyr Glu Met Ser Leu Gln
357     50                  55                  60
359 Ala Phe Asn Ile Phe Ser Gln His Thr Phe Lys Tyr Trp Lys Glu Arg
360 65                  70                  75                  80
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/927,850**

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